

RAW SEQUENCE LISTING

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Application Serial Number: 10/780,043 A
Source: IFW16
Date Processed by STIC: 05/04/2006

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IFW16

RAW SEQUENCE LISTING

DATE: 05/04/2006

PATENT APPLICATION: US/10/780,043A

TIME: 12:02:58

Input Set : A:\10-780,043.txt

Output Set: N:\CRF4\05042006\J780043A.raw

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3 <110> APPLICANT: Bates, Elizabeth
4      Fournier, Nathalie
5      Chalus, Lionel
6      Garrone, Pierre
8 <120> TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND
9      METHODS
11 <130> FILE REFERENCE: SF0977XB
13 <140> CURRENT APPLICATION NUMBER: US 10/780,043A
14 <141> CURRENT FILING DATE: 2004-02-17
15 <150> PRIOR APPLICATION NUMBER: US 09/869,388
17 <151> PRIOR FILING DATE: 1999-12-29
19 <150> PRIOR APPLICATION NUMBER: US 09/223,919
20 <151> PRIOR FILING DATE: 1998-12-31
22 <150> PRIOR APPLICATION NUMBER: US 09/224,604
23 <151> PRIOR FILING DATE: 1998-12-31
25 <160> NUMBER OF SEQ ID NOS: 16
27 <170> SOFTWARE: PatentIn version 3.3
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1249
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (154)..(1062)
39 <220> FEATURE:
40 <221> NAME/KEY: sig_peptide
41 <222> LOCATION: (154)..(210)
43 <220> FEATURE:
44 <221> NAME/KEY: mat_peptide
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50 ctcacctcaa cccccaggcg gccctccac agggccctc tcctgcctgg acggctctgc      120
52 tggctctccc gtcccctgga gaagaacaag gcc atg ggt cgg ccc ctg ctg ctg      174
53                                     Met Gly Arg Pro Leu Leu Leu
54                                     -15
56 ccc cta ctg ccc ctg ctg ctg ccg cca gca ttt ctg cag cct agt ggc      222
57 Pro Leu Leu Pro Leu Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly
58      -10      -5      -1  1
60 tcc aca gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa      270
61 Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys
62 5          10          15          20
64 cac ctc tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc      318

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65 His Leu Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe
66          25          30          35
68 tat tac ccc tgg gag tta gcc aca gct ccc gac gtg aga ata tcc tgg      366
69 Tyr Tyr Pro Trp Glu Leu Ala Thr Ala Pro Asp Val Arg Ile Ser Trp
70          40          45          50
72 aga cgg ggc cac ttc cac ggg cag tcc ttc tac agc aca agg ccg cct      414
73 Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro
74          55          60          65
76 tcc att cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag      462
77 Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu
78          70          75          80
80 ggt cag aag agc ggc ttc ctc agg atc tcc aac ctg cag aag cag gac      510
81 Gly Gln Lys Ser Gly Phe Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp
82 85          90          95          100
84 cag tct gtg tat ttc tgc cga gtt gag ctg gac aca cgg agc tca ggg      558
85 Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Ser Ser Gly
86          105          110          115
88 agg cag cag tgg cag tcc atc gag ggg acc aaa ctc tcc atc acc cag      606
89 Arg Gln Gln Trp Gln Ser Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln
90          120          125          130
92 gct gtc acg acc acc acc cag agg ccc agc agc atg act acc acc tgg      654
93 Ala Val Thr Thr Thr Thr Gln Arg Pro Ser Ser Met Thr Thr Thr Trp
94          135          140          145
96 agg ctc agt agc aca acc acc aca acc ggc ctc agg gtc aca cag ggc      702
97 Arg Leu Ser Ser Thr Thr Thr Thr Thr Gly Leu Arg Val Thr Gln Gly
98          150          155          160
100 aaa cga cgc tca gac tct tgg cac ata agt ctg gag act gct gtg ggg      750
101 Lys Arg Arg Ser Asp Ser Trp His Ile Ser Leu Glu Thr Ala Val Gly
102 165          170          175          180
104 gtg gca gtg gct gtc act gtg ctc gga atc atg att ttg gga ctg atc      798
105 Val Ala Val Ala Val Thr Val Leu Gly Ile Met Ile Leu Gly Leu Ile
106          185          190          195
108 tgc ctc ctc agg tgg agg aga agg aaa ggt cag cag cgg act aaa gcc      846
109 Cys Leu Leu Arg Trp Arg Arg Arg Lys Gly Gln Gln Arg Thr Lys Ala
110          200          205          210
112 aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat gag      894
113 Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu
114          215          220          225
116 aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc aag      942
117 Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys
118          230          235          240
120 gat gac ggc atc gta tat gct tcc ctt gcc ctc tcc agc tcc acc tca      990
121 Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser
122 245          250          255          260
124 ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac gag      1038
125 Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu
126          265          270          275
128 acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa      1092
129 Thr Leu Tyr Ser Val Leu Lys Ala

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130          280
132 tggtagaggcc aggtacagtg ggcacacact gtaatcccag ctactctgaa gcctgaggca 1152
134 gaatcaagtg agcccaggag ttcaggggcca gctttgataa tggagcgaga tgccatctct 1212
136 agttaaaaat atatattaac aataaagtaa caaattt 1249
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 303
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 2
146 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu Pro Pro
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150 Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
151          -1 1          5          10
154 Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
155          15          20          25
158 Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
159 30          35          40          45
162 Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
163          50          55          60
166 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
167          65          70          75
170 Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
171          80          85          90
174 Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
175          95          100          105
178 Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
179 110          115          120          125
182 Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Gln Arg Pro
183          130          135          140
186 Ser Ser Met Thr Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr
187          145          150          155
190 Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile
191          160          165          170
194 Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly
195          175          180          185
198 Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys
199 190          195          200          205
202 Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln
203          210          215          220
206 Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr
207          225          230          235
210 Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu
211          240          245          250
214 Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro Pro Ser His Arg Pro
215          255          260          265
218 Leu Lys Ser Pro Gln Asn Glu Thr Leu Tyr Ser Val Leu Lys Ala
219 270          275          280
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 943

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224 <212> TYPE: DNA
225 <213> ORGANISM: Homo sapiens
228 <220> FEATURE:
229 <221> NAME/KEY: CDS
230 <222> LOCATION: (130)..(819)
232 <220> FEATURE:
233 <221> NAME/KEY: sig_peptide
234 <222> LOCATION: (130)..(180)
236 <220> FEATURE:
237 <221> NAME/KEY: mat_peptide
238 <222> LOCATION: (181)..(819)
240 <400> SEQUENCE: 3
241 acagccctct tcggagcctc agcccggctc tctcactca cctcaacccc caggcggccc      60
243 ctccacaggg cccctctcct gcctggacgg ctctgctggt ctccccgtcc cctggagaag      120
245 aacaaggcc atg ggt cgg ccc ctg ctg ctg ccc cta ctg ccc ctg ctg ctg      171
246      Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu
247      -15_ -10 -5
249 ccg cca gca ttt ctg cag cct agt ggc tcc aca gga tct ggt cca agc      219
250 Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser
251      -1 1 5 10
253 tac ctt tat ggg gtc act caa cca aaa cac ctc tca gcc tcc atg ggt      267
254 Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
255      15 20 25
257 ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta gcc      315
258 Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
259 30 35 40 45
261 aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg      363
262 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Gly His Phe His Gly
263      50 55 60
265 cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat gtg      411
266 Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
267      65 70 75
269 aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc ctc      459
270 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu
271      80 85 90
273 agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc cga      507
274 Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg
275      95 100 105
277 gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc atc      555
278 Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile
279 110 115 120 125
281 gag ggg acc aaa ctc tcc atc acc cag ggt cag cag cgg act aaa gcc      603
282 Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys Ala
283      130 135 140
285 aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat gag      651
286 Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu
287      145 150 155
289 aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc aag      699
290 Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys

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291          160          165          170
293 gat gac ggc atc gtc tat gct tcc ctt gcc ctc tcc agc tcc acc tca      747
294 Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser
295          175          180          185
297 ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac gag      795
298 Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu
299 190          195          200          205
301 acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa      849
302 Thr Leu Tyr Ser Val Leu Lys Ala
303          210
305 tgggtgaggcc aggtacagtg ggcacacact gtaatcccag ctactctgaa gcctgaggca      909
307 gaatcaagtg agcccaggag ttcagggcca gctt      943
310 <210> SEQ ID NO: 4
311 <211> LENGTH: 230
312 <212> TYPE: PRT
313 <213> ORGANISM: Homo sapiens
315 <400> SEQUENCE: 4
317 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu Pro Pro
318          -15          -10          -5
321 Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
322 -1 1          5          10          15
325 Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
326          20          25          30
329 Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
330          35          40          45
333 Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
334          50          55          60
337 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
338          65          70          75
341 Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
342 80          85          90          95
345 Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
346          100          105          110
349 Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
350          115          120          125
353 Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys Ala Thr Thr
354          130          135          140
357 Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu Asn Ile
358          145          150          155
361 Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys Asp Asp
362 160          165          170          175
365 Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser Pro Arg
366          180          185          190
369 Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu Thr Leu
370          195          200          205
373 Tyr Ser Val Leu Lys Ala
374          210
377 <210> SEQ ID NO: 5
378 <211> LENGTH: 1450

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VERIFICATION SUMMARY

DATE: 05/04/2006

PATENT APPLICATION: US/10/780,043A

TIME: 12:02:59

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